

BASE COUNT 154 a 90 c 136 g 93 t 2 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.000785 Length: 475
 Score: 69.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-856-070-17 (1-14) x AF189213 (1-475)

QY 1 GluArgGluIysGluMetMetArgGluIysGluGluLeu 14
 |||||
 DB 410 GACAGACAAAGACACATGATGCGGAGAGAGGAGGATG 451

RESULT 4

AF189213
 LOCUS Homo sapiens ezrin mRNA, partial cds.
 DEFINITION AF189213
 ACCESSION AF189213
 VERSION AF189213.1 GI:6063146
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM
 Eukaryota; Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
 Mammalia; Eutheria; Primates, Catarrhini, Hominoidea, Homo.
 Fadiel, A., Chen, Z.-C. and Naftolins, F.
 1 (bases 1 to 478)
 Mutation of ezrin gene in cancer
 JOURNAL
 TITLE Unpublished
 REFERENCE 2 (bases 1 to 478)
 Fadiel, A., Chen, Z.-C. and Naftolins, F.
 Direct Submission
 TITLE
 JOURNAL Submitted (23-SEP-1999) CB/SYN, Yale University, 333 Cedar Street,
 New Haven, CT 06520, USA

FEATURES
 source
 Location/Qualifiers
 1..478
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6q22-q27"
 /cell_line="HL60"
 /tissue_type="leukemia cells"
 /note="villin 2: kinase substrate"
 /codon_start=2
 /product="ezrin"
 /protein_id="AA03156.1"
 /db_xref="GI:6063147"

CDS
 1..478
 /note="villin 2: kinase substrate"
 /codon_start=2
 /product="ezrin"
 /protein_id="AA03156.1"
 /db_xref="GI:6063147"

BASE COUNT 154 a 90 c 136 g 93 t 2 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.00079 Length: 478
 Score: 69.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-856-070-17 (1-14) x AF189213 (1-478)

QY 1 GluArgGluIysGluMetMetArgGluIysGluGluLeu 14
 |||||
 DB 410 GACAGACAAAGACACATGATGCGGAGAGAGGAGGATG 451

RESULT 5

AF187552
 LOCUS Homo sapiens ezrin mRNA, partial cds.
 DEFINITION AF187552
 ACCESSION AF187552
 VERSION AF187552.1 GI:5930070
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM
 Eukaryota; Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
 Mammalia; Eutheria; Primates, Catarrhini, Hominoidea, Homo.
 Chen, Z.-C., Fadiel, A. and Naftolins, F.
 1 (bases 1 to 489)
 Mutation analysis of ezrin gene in cancer cells
 JOURNAL
 TITLE Unpublished (1999)
 REFERENCE 2 (bases 1 to 489)
 Chen, Z.-C., Fadiel, A. and Naftolins, F.
 Direct Submission
 TITLE
 JOURNAL Submitted (16-SEP-1999) CB/SYN, Yale University, 333 Cedar Street,
 New Haven, CT 06511, USA

FEATURES
 source
 Location/Qualifiers
 1..489
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6q22-q27"
 /tissue_type="placenta"
 /note="villin 2: Cvt"
 /codon_start=2
 /product="ezrin"
 /protein_id="AAU56713.1"
 /db_xref="GI:5930071"

CDS
 1..489
 /note="villin 2: Cvt"
 /codon_start=2
 /product="ezrin"
 /protein_id="AAU56713.1"
 /db_xref="GI:5930071"

BASE COUNT 158 a 93 c 140 g 95 t 2 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.00080 Length: 489
 Score: 69.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-856-070-17 (1-14) x AF187552 (1-489)

QY 1 GluArgGluIysGluMetMetArgGluIysGluGluLeu 14
 |||||
 DB 428 GACAGACAAAGACACATGATGCGGAGAGAGGAGGATG 469

RESULT 6

BOVEZPINA
 LOCUS Bos taurus ezrin mRNA, complete cds.
 DEFINITION M98498
 ACCESSION M98498.1 GI:289407
 VERSION
 KEYWORDS ezrin.
 SOURCE Bos taurus
 ORGANISM
 Eukaryota; Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla, Ruminantia, Pecora; Bovidae;
 Bovinae; Bos.
 1 (bases 1 to 2514)
 Ezrin and osteonectin, two proteins associated with cell shape and
 growth, are enriched in the locus coeruleus
 JOURNAL
 TITLE Mol. Cell. Neurosci. 4, 64-73 (1993)
 FEATURES
 source
 Location/Qualifiers
 1..2514
 /organism="Bos taurus"

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/tissue_type="brain"
152..1847
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NKKIIGICMNHKE.YVRRKKPDIIEVOOMKAQREKHOKIQRQLEIYKRRRTVE
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EKKRTEAKENKRVQMLTISELSQADENKTHINDIINENMPQSPYKTIPLQI
KQCNTRIDDEPAM"
BASE COUNT 644 a 658 c 738 q 474 t
ORIGIN

Alignment Scores:
Pred. No.: 0.00431 Length: 2514
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-856-070-17 (1-14) x H0VZFPIINA (1-2514)

QY 1 GluArgGluLysGluGlnMetMetArgGluLysGluGluLeu 14
Db 1151 GAGGCAAAAAGACATGATGCTGTAAGAGAGAGACTG 1192
RESULT 7
LOCUS HUMV112
DEFINITION Human cytoovillin 2 (VIL2) mRNA, complete cds.
ACCESSION J05021
VERSION J05021.1 GI:340216
KEYWORDS cytoovillin; cytoovillin 2; microvilliar protein.
SOURCE Human placenta, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Turunen,O., Winqvist,R., Pakkanen,R., Grzeschik,K.H., Wahlstrom,T.
and Vaheri,A.
TITLE Cytoovillin, a microvilliar Mr 75,000 protein, cDNA sequence,
prokaryotic expression, and chromosomal localization
JOURNAL J. Biol. Chem. 264 (28), 16727-16732 (1989)
MEDLINE 89480299
PMID 2674140
COMMENT Draft entry and computer readable sequence for [1] kindly submitted
by O.Turunen, 31-AUG-1989.
FEATURES
Source
Location/Qualifiers
1..2530
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6q22-q27"
1..2530
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110..1837
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/translation="MTAFIEPATQNTTQKLPDQVWVTIGLPEWVYFSLIYVKNKGF
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10VHAHHRMILKUNAMELYKLAQELMWMYQINYEIEKKKCTIDELWGLQALQNLVE
KQKLEKLGFWSEIKNISNKAHYVAPLKKRAHVEVAPRLKIKRKLQCMGN
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ERQAVDIKSEQALAEAYTAKIALLEEAREKKEDEVEEWHRAEQADQLYKRE
ELHLVMTAPPDPVYVYVHIESQADENKTHINDIINENMPQSPYKTIPLQI
EKKRTEAKENKRVQMLTISELSQADENKTHINDIINENMPQSPYKTIPLQI
KQCNTRIDDEPAM"
BASE COUNT 793 a 658 c 821 q 658 t
ORIGIN

Alignment Scores:
Pred. No.: 0.00504 Length: 2940
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-856-070-17 (1-14) x HUMV112 (1-2940)

QY 1 GluArgGluLysGluGlnMetMetArgGluLysGluGluLeu 14
Db 1076 GAGAGACAGAAACAGTACATCATGCGGAGAGAGAGTIG 1117
RESULT 8
LOCUS AX411074
DEFINITION Sequence 3721 from Patent W00229103.
ACCESSION AX411074
VERSION AX411074.1 GI:21443779
KEYWORDS human.
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Alvarado,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 3721 11-APR-2002;
GENE LOGIC INC (US)
FEATURES
Source
Location/Qualifiers
1..3044
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="EMBL/GenBank Accession No. X51521"
BASE COUNT 826 a 687 c 855 q 675 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 0.00524 Length: 4044
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-17 (1-14) x AX411074 (1-3044)

QY 1 GluArgGluLysGluGlnMetMetArgGluLysGluGluLeu 14
Db 1117 GAGAGACAGAAACAGTACATCATGCGGAGAGAGAGTIG 1158
RESULT 9
LOCUS HSEZRIN
DEFINITION Human mRNA for ezrin.
ACCESSION X51521
VERSION X51521.1 GI:31282
KEYWORDS ezrin; kinase substrate, microvilli protein.
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS HSEZRIN
TITLE Human mRNA for ezrin.
JOURNAL X51521
VERSION X51521.1 GI:31282
KEYWORDS ezrin; kinase substrate, microvilli protein.
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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 KUTRKGFPNSFTNINSEKKEVFKPIKKKAPDVFYAPPLPINKPIIQLMGNIHEL
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 AVQIQSQEYLAEALRYAKIALIIEAKRKEDRVEWHRKRAQADQIVYKTKRELH
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 DEFEAL"

polyA_signal 3042..3037

polyA_site 3051

BASE COUNT 846 a 688 c 868 g 670 t

ORIGIN

Alignment Scores:

Aligned No.: 0.00529 Length: 3072
 Score: 69.00 Matches: 14
 Percent Similarity: 100.00% Conservatively: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-856-070-17 (1-14) x HSM802625 (1-3072)

QY 1 GluArgGluIysGluMetMetArgGluIysGluGluLeu 14

|||||

Db 1143 GAGAGAGAGAAAGACATGATGATGAGAGAGAGAGAGGTTG 1174

RESULT 12

LOCUS BC013903

DEFINITION Homo cap.cds, similar to villin 2 (villin), clone MGC-1584
 IMAGE:2959399, mRNA, complete cds.

ACCESSION BC013903

VERSION BC013903.1 GI:15530242

KEYWORDS MGC

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 3174)

Strausberg, R.

Direct Submission

Submitted (07-SEP-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A04, Bethesda, MD 20892, USA

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cdaps-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Pubin Laboratory

cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadan@systemsbiology.org

Anup Madan, Rachel Buckleff, Jessica Pahey, Stephanie Ford, Julia

Greene, Mark Kettman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 2 Row: a Column: 18

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 9257254.

Location/Qualifiers

1..3173

FEATURES

SOURCE

organism="Homo sapiens"

db_xref="taxon:9606"

clone="MGC1584 IMAGE:2959399"

feature_type="cds, coding, adjacent_coding"

clone_lib="NIH_MGC_15"

lab_host="DH10B-R"

/note="Vector: p01H7"

142..1902

/codon_start=1

/product="Similar to villin 2 (villin)"

/protein_id="AAH13903.1"

/db_xref="GI:15530243"

/translation="MKPKINVRVTIMAFLEAFQINLIGKQLPQVVKTLGLREVWY

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NKKILQIGMGNHLYMKRKKIKIILVQOMKQAPEKRIKQERQOETETEKRPETVE

REKQMMREKEELMLIODYEKTKKAPRELQIRALQIERKRAQERKRIKADRMALRA

EMAALRAKPELEHQAVIDIKSQPOLAALAEVYAKIALIIEAKRKEDRVEWHRKRA

EQDDLVTKEELILVMATAPPVPPPPVYVSVYVGVTSIQCTAPITQYSALIESVGIP

QBNFERRPITAEKNEFVQVQULLTISSELSQAPFNKPTIUNIIINENMPGKPKYK

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BASE COUNT 930 a 691 c 868 g 684 t

ORIGIN

Alignment Scores:

Aligned No.: 0.00547 Length: 4173
 Score: 69.00 Matches: 14
 Percent Similarity: 100.00% Conservatively: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-856-070-17 (1-14) x BC013903 (1-3173)

QY 1 GluArgGluIysGluMetMetArgGluIysGluGluLeu 14

|||||

Db 1143 GAGAGAGAGAAAGACATGATGATGAGAGAGAGAGGTTG 1182

RESULT 13

LOCUS AL589931

DEFINITION Human DNA sequence from clone RP11-507C10 on chromosome 6q25.2-26.

complete sequence.

AL589931 AC024785

AL589931.14 GI:15591370

KEYWORDS HIG.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 215705)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (15-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

requests: clonerequest@sanger.ac.uk

On Sep 12, 2001 this sequence version replaced gi:14586248.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M14 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: EMBL, EMBL; SW,

SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP

database can be found at

http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human

chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping

100

Search completed: January 16, 2003, 19:02:38
Job time : 1248.6 secs